

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/517,491A  
Source: IFW/6  
Date Processed by STIC: 4/12/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 04/12/2005

PATENT APPLICATION: US/09/517,491A

TIME: 14:20:54

Input Set : A:\ABPI-P06-036.TXT

Output Set: N:\CRF4\04122005\I517491A.raw

4 <110> APPLICANT: Berlin, Vivian  
 5 Chiu, Maria Isabel  
 6 Cottarel, Guillaume  
 7 Damagnez, Veronique  
 9 <120> TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS  
 12 <130> FILE REFERENCE: APBI-P06-036  
 14 <140> CURRENT APPLICATION NUMBER: US 09/517,491A  
 15 <141> CURRENT FILING DATE: 2000-03-02  
 17 <150> PRIOR APPLICATION NUMBER: US 08/360,144  
 18 <151> PRIOR FILING DATE: 1994-12-20  
 20 <150> PRIOR APPLICATION NUMBER: US 08/250,795  
 21 <151> PRIOR FILING DATE: 1994-05-27  
 23 <160> NUMBER OF SEQ ID NOS: 35  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 486  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Mouse  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)...(486)  
 36 <400> SEQUENCE: 1

37	ctc acc cgt cac aat gca gcc aac aag atc ttg aag aac atg tgt gaa	48
38	Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu	
39	1 5 10 15	
41	cac agc aac acg ctg gtc cag cag gcc atg atg gtg agt gaa gag ctg	96
42	His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu	
43	20 25 30	
45	att cgg gta gcc atc ctc tgg cat gag atg tgg cat gaa ggc ctg gaa	144
46	Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu	
47	35 40 45	
49	gag gca tct cgc ttg tac ttt ggg gag agg aac gtg aaa ggc atg ttt	192
50	Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe	
51	50 55 60	
53	gag gtg ctg gag ccc ctg cat gct atg atg gaa cgg ggt ccc cgg act	240
54	Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr	
55	65 70 75 80	
57	ctg aag gaa aca tcc ttt aat cag gca tat ggc cga gat tta atg gag	288
58	Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu	
59	85 90 95	
61	gca caa gaa tgg tgt cga aag tac atg aag tcg ggg aac gtc aag gac	336
62	Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp	
63	100 105 110	

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```

65 ctc acg caa gcc tgg gac ctc tac tat cac gtg ttc aga cgg atc tca 384
66 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
67      115      120      125
69 aag cag cta ccc cag ctc aca tcc ctg gag ctg cag tat gtg tcc ccc 432
70 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
71      130      135      140
73 aaa ctt ctg atg tgc cga gac ctt gag ttg gct gtg cca gga aca tac 480
74 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
75 145      150      155      160
77 gac ccc 486
78 Asp Pro
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 162
84 <212> TYPE: PRT
85 <213> ORGANISM: Mouse
87 <400> SEQUENCE: 2
88 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
89 1      5      10      15
90 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
91      20      25      30
92 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
93      35      40      45
94 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
95      50      55      60
96 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
97 65      70      75      80
98 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
99      85      90      95
100 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
101      100      105      110
102 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
103      115      120      125
104 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
105      130      135      140
106 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
107 145      150      155      160
108 Asp Pro
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 40
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: oligonucleotide
120 <400> SEQUENCE: 3
121 gggtttggaattcctaataa tgtctgtaca agtagaaacc 40
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 34
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence

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```

128 <220> FEATURE:
129 <223> OTHER INFORMATION: oligonucleotide
131 <400> SEQUENCE: 4
132 gggtttcggg atcccgatcat tccagtttta gaac 34
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 348
136 <212> TYPE: DNA
137 <213> ORGANISM: Homo sapiens
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (14)...(325)
143 <400> SEQUENCE: 5
144 ggaattccta ata atg tcc gta caa gta gaa acc atc tcc cca gga gac 49
145 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
146 1 5 10
148 ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc 97
149 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
150 15 20 25
152 ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac 145
153 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
154 30 35 40
156 aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg 193
157 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
158 45 50 55 60
160 gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act 241
161 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
162 65 70 75
164 ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc 289
165 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
166 80 85 90
168 cca cca cat gcc act ctc gtc ttc gat gtg gag ctt ctaaaactgg 335
169 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
170 95 100
172 aatgacggga tcc 348
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 104
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 6
180 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
181 1 5 10 15
182 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
183 20 25 30
184 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
185 35 40 45
186 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
187 50 55 60
188 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
189 65 70 75 80

```

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190 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
191      85                      90                      95
192 Thr Leu Val Phe Asp Val Glu Leu
193      100
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 48
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: oligonucleotide
204 <400> SEQUENCE: 7
205 tcgccggaat tcgggggcgg aggtggagga gtacaagtag aaaccatc      48
207 <210> SEQ ID NO: 8
208 <211> LENGTH: 34
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: oligonucleotide
215 <400> SEQUENCE: 8
216 gggtttcggg atcccgatcat tccagtttta gaag      34
218 <210> SEQ ID NO: 9
219 <211> LENGTH: 41
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: oligonucleotide
226 <400> SEQUENCE: 9
227 cgcggatccg cgcattatta cttgttttga ttgatttttt g      41
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 40
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: oligonucleotide
237 <400> SEQUENCE: 10
238 cgcggatccg cgtaaaagca aagtactatc aattgagccg      40
240 <210> SEQ ID NO: 11
241 <211> LENGTH: 5430
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)...(5427)
249 <400> SEQUENCE: 11
250 ttg gag cac agt ggg att gga aga atc aaa gag cag agt gcc cgc atg      48
251 Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
252 1      5      10      15
254 ctg ggg cac ctg gtc tcc aat gcc ccc cga ctc atc cgc ccc tac atg      96
255 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met

```

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256		20		25		30		
258	gag	cct	att	ctg	aag	gca	tta	att
259	Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile
260			35			40		45
262	gat	cca	aac	cca	ggt	gtg	atc	aat
263	Asp	Pro	Asn	Pro	Gly	Val	Ile	Asn
264		50			55		60	
266	ttg	gca	cag	gtt	agt	ggc	ctg	gaa
267	Leu	Ala	Gln	Val	Ser	Gly	Leu	Glu
268	65				70		75	80
270	ttt	att	atc	atc	atg	gac	atg	ctc
271	Phe	Ile	Ile	Ile	Met	Asp	Met	Leu
272					85		90	95
274	agg	cag	gtg	gct	ctg	tggt	acc	ctg
275	Arg	Gln	Val	Ala	Leu	Trp	Thr	Leu
276			100			105		110
278	tat	gta	gta	gag	ccc	tac	agg	aag
279	Tyr	Val	Val	Glu	Pro	Tyr	Arg	Lys
280			115			120		125
282	ctg	aat	ttt	ctg	aag	act	gag	cag
283	Leu	Asn	Phe	Leu	Lys	Thr	Glu	Gln
284		130				135		140
286	atc	cgt	gtg	tta	ggg	ctt	tta	ggg
287	Ile	Arg	Val	Leu	Gly	Leu	Leu	Gly
288	145				150		155	160
290	gtg	aac	att	ggc	atg	ata	gac	cag
291	Val	Asn	Ile	Gly	Met	Ile	Asp	Gln
292				165			170	175
294	ctg	tca	gaa	tcc	aag	tca	agt	cag
295	Leu	Ser	Glu	Ser	Lys	Ser	Ser	Gln
296			180			185		190
298	gaa	atg	ctg	gtc	aac	atg	gga	aac
299	Glu	Met	Leu	Val	Asn	Met	Gly	Asn
300		195				200		205
302	gct	gtg	tcc	atg	gtg	gcc	ctg	atg
303	Ala	Val	Ser	Met	Val	Ala	Leu	Met
304		210				215		220
306	tct	cat	cat	cac	acc	atg	gtt	gtc
307	Ser	His	His	His	Thr	Met	Val	Val
308	225				230		235	240
310	tcc	ctg	gga	ctc	aaa	tgt	gtg	cag
311	Ser	Leu	Gly	Leu	Lys	Cys	Val	Gln
312				245			250	255
314	ttc	ctt	aat	gtc	att	cga	gtc	tgt
315	Phe	Leu	Asn	Val	Ile	Arg	Val	Cys
316			260			265		270
318	ttc	cag	cag	ctg	gga	atg	ttg	gtg
319	Phe	Gln	Gln	Leu	Gly	Met	Leu	Val
320			275			280		285

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 04/12/2005  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 59,64,72,74,89,94,101,137,158,175,190,201,207,210,213,218  
Seq#:19; N Pos. 234,243,257,283,286,289,292,314,325,328,335,352,361,380,384  
Seq#:19; N Pos. 390,393,403,411,413,427,432,435,440,443,450,452,460,465,480  
Seq#:19; N Pos. 482,486,492,515  
Seq#:23; N Pos. 27,373,443,461,483,485,507,583,588,593,605,606,607,612,624  
Seq#:23; N Pos. 625,626,627,628,630,631,632,635,639,646,652,659,661  
Seq#:24; Xaa Pos. 105  
Seq#:25; N Pos. 112,148,158,171,178,182,191,194,203,204  
Seq#:29; N Pos. 3,9,15  
Seq#:30; N Pos. 3,6,21

## VERIFICATION SUMMARY

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L:1157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
M:341 Repeated in SeqNo=19  
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0  
M:341 Repeated in SeqNo=23  
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:96  
L:1264 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:1268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25  
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:60  
M:341 Repeated in SeqNo=25  
L:1312 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:1316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29  
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0  
L:1327 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:1331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0